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1636

TECH CENTER 1600/2900



1600

RAW SEQUENCE LISTING

DATE: 07/31/2002

PATENT APPLICATION: US/09/696,867

TIME: 14:43:11

Input Set : A:\501d6.app

Output Set: N:\CRF3\07312002\I696867.raw

#11

p.6

4 <110> APPLICANT: Brunkow, Mary E.
 5 Jeffery, Eric W.
 6 Hjerrild, Kathryn A.
 7 Ramsdell, Fred
 11 <120> TITLE OF INVENTION: IDENTIFICATION OF THE GENE CAUSING THE
 12 MOUSE SCURFY PHENOTYPE AND ITS HUMAN ORTHOLOG
 15 <130> FILE REFERENCE: 240083.501D6
 17 <140> CURRENT APPLICATION NUMBER: US 09/696,867
 18 <141> CURRENT FILING DATE: 2000-10-25
 20 <160> NUMBER OF SEQ ID NOS: 14
 22 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 2160
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Mus musculus
 29 <400> SEQUENCE: 1

ENTERED

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31	ccagacacag	ctctgctggc	gaaagtggca	gagaggatt	gaggggtggg	gtcaggagcc	120
32	caccagtaca	gctggaaaca	cccagccact	ccagctcccg	gcaacttctc	ctgactctgc	180
33	cttcagacga	gacttgggaag	acagtcacat	ctcagcagct	cctctgccgt	tatccagcct	240
34	gcctctgaca	agaacccaat	gccccaccct	aggccagcca	agcctatggc	tccttccttg	300
35	gccccttgcc	catccccagg	agtcttgcca	agctgggaaga	ctgcacccaa	gggctcagaa	360
36	cttctaggga	ccaggggctc	tgggggaccc	ttccaagggtc	gggacctgcg	aagtggggcc	420
37	cacacctctt	cttccctgaa	ccccctgcca	ccatcccagc	tgcagctgcc	tacagtgtcc	480
38	ctagtcatgg	tggcaccgtc	tggggcccga	ctaggtccct	caccccacct	acaggccctt	540
39	ctccaggaca	gaccacactt	catgcatcag	ctctccactg	tggatgcca	tgcccagacc	600
40	cctgtgctcc	aagtgcgtcc	actggacaac	ccagccatga	tcagcctccc	accaccttct	660
41	gctgccactg	gggtcttctc	cctcaaggcc	cggcctggcc	tgccacctgg	gatcaatgtg	720
42	gccagtctgg	aatgggtgtc	cagggagcca	gctctactct	gcaccttccc	acgctcgggt	780
43	acaccagga	aagacagcaa	ccttttggtc	gcaccccaag	gatcctaccc	actgctggca	840
44	aatggagtct	gcaagtggcc	tggttgtgag	aaggtcttcg	aggagccaga	agagtttctc	900
45	aagcactgcc	aagcagatca	tctcctggat	gagaaaggca	aggcccagtg	cctcctccag	960
46	agagaagtgg	tgcagtctct	ggagcagcag	ctggagctgg	aaaaggagaa	gctgggagct	1020
47	atgcaggccc	acctggctgg	gaagatggcg	ctggccaagg	ctccatctgt	ggcctcaatg	1080
48	gacaagagct	cttgctgcac	cgtagccacc	agtactcagg	gcagtgtgct	cccggcctgg	1140
49	tctgtctctc	gggaggctcc	agacggcggc	ctggttgacg	tgcggaggca	cctctgggga	1200
50	agccatggca	atagttcctt	cccagagttc	ttccacaaca	tggactactt	caagtaccac	1260
51	aatatgcgac	ccccctttcac	ctatgccacc	cttatccgat	gggccatcct	ggaagccccg	1320
52	gagaggcaga	ggacactcaa	tgaatctac	catttggttta	ctcgcagtgt	cgcctacttc	1380
53	agaaaccacc	ccgccacctg	gaagaatgcc	atccgccaca	acctgagcct	gcacaagtgc	1440
54	tttgtgcgag	tggagagcga	gaagggagca	gtgtggaccg	tagatgaatt	tgagtttcgc	1500
55	aagaagagga	gccaacgccc	caacaagtgc	tccaatccct	gcccttgacc	tcaaaaccaa	1560
56	gaaaaggtgg	gcggggggagg	gggccaaaac	catgagactg	aggctgtggg	ggcaaggagg	1620

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57 caagtcctac gtgtacctat ggaaaccggg cgatgatgtg cctgctatca gggcctctgc 1680
58 tccctatcta gctgccctcc tagatcatat catctgcctt acagctgaga ggggtgccaa 1740
59 tcccagccta gcccctagtt ccaacctagc cccaagatga actttccagt caaagagccc 1800
60 tcacaaccag ctatacatat ctgccttggc cactgccaag cagaaagatg acagacacca 1860
61 tcctaataatt tactcaacccc aaacctataa acatgaagag cctgccttgg tacattcgtg 1920
62 aactttcaaaa gttagtcatg cagtcacaca tgactgcagt cctactgact cacaccccaa 1980
63 agcactcacc cacaacatct ggaaccacgg gcactatcac acataggtgt atatacagac 2040
64 ccttacacag caacagcact ggaaccttca caattacatc cccccaacc acacaggcat 2100
65 aactgatcat acgcagcctc aagcaatgcc caaaatacaa gtcagacaca gcttgctcaga 2160
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68 <211> LENGTH: 429
69 <212> TYPE: PRT
70 <213> ORGANISM: Mus musculus
72 <400> SEQUENCE: 2
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74 1 5 10 15
75 Gly Pro Ser Pro Gly Val Leu Pro Ser Trp Lys Thr Ala Pro Lys Gly
76 20 25 30
77 Ser Glu Leu Leu Gly Thr Arg Gly Ser Gly Gly Pro Phe Gln Gly Arg
78 35 40 45
79 Asp Leu Arg Ser Gly Ala His Thr Ser Ser Ser Leu Asn Pro Leu Pro
80 50 55 60
81 Pro Ser Gln Leu Gln Leu Pro Thr Val Pro Leu Val Met Val Ala Pro
82 65 70 75 80
83 Ser Gly Ala Arg Leu Gly Pro Ser Pro His Leu Gln Ala Leu Leu Gln
84 85 90 95
85 Asp Arg Pro His Phe Met His Gln Leu Ser Thr Val Asp Ala His Ala
86 100 105 110
87 Gln Thr Pro Val Leu Gln Val Arg Pro Leu Asp Asn Pro Ala Met Ile
88 115 120 125
89 Ser Leu Pro Pro Pro Ser Ala Ala Thr Gly Val Phe Ser Leu Lys Ala
90 130 135 140
91 Arg Pro Gly Leu Pro Pro Gly Ile Asn Val Ala Ser Leu Glu Trp Val
92 145 150 155 160
93 Ser Arg Glu Pro Ala Leu Leu Cys Thr Phe Pro Arg Ser Gly Thr Pro
94 165 170 175
95 Arg Lys Asp Ser Asn Leu Leu Ala Ala Pro Gln Gly Ser Tyr Pro Leu
96 180 185 190
97 Leu Ala Asn Gly Val Cys Lys Trp Pro Gly Cys Glu Lys Val Phe Glu
98 195 200 205
99 Glu Pro Glu Glu Phe Leu Lys His Cys Gln Ala Asp His Leu Leu Asp
100 210 215 220
101 Glu Lys Gly Lys Ala Gln Cys Leu Leu Gln Arg Glu Val Val Gln Ser
102 225 230 235 240
103 Leu Glu Gln Gln Leu Glu Leu Glu Lys Glu Lys Leu Gly Ala Met Gln
104 245 250 255
105 Ala His Leu Ala Gly Lys Met Ala Leu Ala Lys Ala Pro Ser Val Ala
106 260 265 270
107 Ser Met Asp Lys Ser Ser Cys Cys Ile Val Ala Thr Ser Thr Gln Gly

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108          275          280          285
109 Ser Val Leu Pro Ala Trp Ser Ala Pro Arg Glu Ala Pro Asp Gly Gly
110          290          295          300
111 Leu Phe Ala Val Arg Arg His Leu Trp Gly Ser His Gly Asn Ser Ser
112 305          310          315          320
113 Phe Pro Glu Phe Phe His Asn Met Asp Tyr Phe Lys Tyr His Asn Met
114          325          330          335
115 Arg Pro Pro Phe Thr Tyr Ala Thr Leu Ile Arg Trp Ala Ile Leu Glu
116          340          345          350
117 Ala Pro Glu Arg Gln Arg Thr Leu Asn Glu Ile Tyr His Trp Phe Thr
118          355          360          365
119 Arg Met Phe Ala Tyr Phe Arg Asn His Pro Ala Thr Trp Lys Asn Ala
120          370          375          380
121 Ile Arg His Asn Leu Ser Leu His Lys Cys Phe Val Arg Val Glu Ser
122 385          390          395          400
123 Glu Lys Gly Ala Val Trp Thr Val Asp Glu Phe Glu Phe Arg Lys Lys
124          405          410          415
125 Arg Ser Gln Arg Pro Asn Lys Cys Ser Asn Pro Cys Pro
126          420          425

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128 <210> SEQ ID NO: 3

129 <211> LENGTH: 1869

130 <212> TYPE: DNA

131 <213> ORGANISM: Homo sapien

133 <400> SEQUENCE: 3

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135 cgtacagcgt ggtttttctt ctcggtataa aagcaaagtt gtttttgata cgtgacagtt      120
136 tcccacaagc caggctgata cttttctgtc agtccacttc accaagcctg cccttggaca      180
137 aggacccgat gcccaacccc aggcctggca agccctcggc cccttccttg gcccttggcc      240
138 catccccagg agcctcgccc agctggaggg ctgcacccaa agcctcagac ctgctggggg      300
139 cccggggccc agggggaacc ttccagggcc gagatcttcg aggcggggcc catgcctcct      360
140 cttcttcctt gaaccccatg ccaccatcgc agctgcagct gccacactg cccctagtca      420
141 tgggtggcacc ctccggggca cggctggggc ccttgcccca cttacaggca ctctccagg      480
142 acaggccaca ttcatgcac cagctctcaa cgggtggatgc ccacgcccgg acccctgtgc      540
143 tgcaggtgca ccccttgag agcccagcca tgcacagcct cacaccaccc accaccgcca      600
144 ctgggggtctt ctccctcaag gcccggcctg gcctcccacc tgggatcaac gtggccagcc      660
145 tggaatgggt gtccaggag cgggcactgc tctgcacctt cccaaatccc agtgacacca      720
146 ggaaggacag caccctttcg gctgtgcccc agagctccta cccactgctg gcaaagtgtg      780
147 tctgcaagtg gcccgatgt gagaaggtct tcgaagagcc agaggacttc ctcaagcact      840
148 gccaggcgga ccatcttctg gatgagaagg gcagggcaca atgtctcctc cagagagaga      900
149 tggtagagtc tctggagcag cagctggtgc tggagaagga gaagctgagt gccatgcagg      960
150 cccacctggc tgggaaaatg gcactgacca aggccttcac tgtggcatca tccgacaagg      1020
151 gctcctgctg catcgtagct gctggcagcc aaggccctgt cgtcccagcc tggcttgggc      1080
152 cccggggagg ccttgacagc ctgtttgctg tccggaggca cctgtggggg agccatggaa      1140
153 acagcacatt cccagagttc ctccacaaca tggactactt caagttccac aacatgcgac      1200
154 cccctttcac ctacgccag ctcatccgct gggccatcct ggaggctcca gagaagcagc      1260
155 ggacactcaa tgagatctac cactggttca cacgcatgtt tgctttcttc agaaaccatc      1320
156 ctgccacctg gaagaacgcc atccgccaca acctgagttc gcacaagtgc tttgtgcggg      1380
157 tggagagcga gaagggggct gtgtggaccg tggatgagct ggagttccgc aagaaacgga      1440
158 gccagaggcc cagcaggtgt tocaacccta cacctggccc ctgacctcaa gatcaaggaa      1500

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159  aggaggatgg  acgaacaggg  gccaaactgg  tgggaggcag  aggtggtggg  ggcagggatg  1560
160  ataggccctg  gatgtgcca  cagggacca  gaagtggagt  ttccactgtc  ttgcctgcca  1620
161  gggccctgt  tccccgctg  gcagccacc  cctcccccat  catatccttt  gcccgaaggc  1680
162  tgctcagagg  ggccccggtc  ctggccccag  cccccacctc  cgccccagac  acacccccca  1740
163  gtcgagccct  gcagccaaac  agagccttca  caaccagcca  cacagagcct  gcctcagctg  1800
164  ctcgcacaga  ttacttcagg  gctggaaaag  tcacacagac  acacaaaatg  tcacaatcct  1860
165  gtccctcac                                     1869
167 <210> SEQ ID NO: 4
168 <211> LENGTH: 431
169 <212> TYPE: PRT
170 <213> ORGANISM: Homo sapien
172 <400> SEQUENCE: 4
173  Met Pro Asn Pro Arg Pro Gly Lys Pro Ser Ala Pro Ser Leu Ala Leu
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175  Gly Pro Ser Pro Gly Ala Ser Pro Ser Trp Arg Ala Ala Pro Lys Ala
176              20              25              30
177  Ser Asp Leu Leu Gly Ala Arg Gly Pro Gly Gly Thr Phe Gln Gly Arg
178              35              40              45
179  Asp Leu Arg Gly Gly Ala His Ala Ser Ser Ser Ser Leu Asn Pro Met
180              50              55              60
181  Pro Pro Ser Gln Leu Gln Leu Pro Thr Leu Pro Leu Val Met Val Ala
182              65              70              75              80
183  Pro Ser Gly Ala Arg Leu Gly Pro Leu Pro His Leu Gln Ala Leu Leu
184              85              90              95
185  Gln Asp Arg Pro His Phe Met His Gln Leu Ser Thr Val Asp Ala His
186              100             105             110
187  Ala Arg Thr Pro Val Leu Gln Val His Pro Leu Glu Ser Pro Ala Met
188              115             120             125
189  Ile Ser Leu Thr Pro Pro Thr Thr Ala Thr Gly Val Phe Ser Leu Lys
190              130             135             140
191  Ala Arg Pro Gly Leu Pro Pro Gly Ile Asn Val Ala Ser Leu Glu Trp
192              145             150             155             160
193  Val Ser Arg Glu Pro Ala Leu Leu Cys Thr Phe Pro Asn Pro Ser Ala
194              165             170             175
195  Pro Arg Lys Asp Ser Thr Leu Ser Ala Val Pro Gln Ser Ser Tyr Pro
196              180             185             190
197  Leu Leu Ala Asn Gly Val Cys Lys Trp Pro Gly Cys Glu Lys Val Phe
198              195             200             205
199  Glu Glu Pro Glu Asp Phe Leu Lys His Cys Gln Ala Asp His Leu Leu
200              210             215             220
201  Asp Glu Lys Gly Arg Ala Gln Cys Leu Leu Gln Arg Glu Met Val Gln
202              225             230             235             240
203  Ser Leu Glu Gln Gln Leu Val Leu Glu Lys Glu Lys Leu Ser Ala Met
204              245             250             255
205  Gln Ala His Leu Ala Gly Lys Met Ala Leu Thr Lys Ala Ser Ser Val
206              260             265             270
207  Ala Ser Ser Asp Lys Gly Ser Cys Cys Ile Val Ala Ala Gly Ser Gln
208              275             280             285
209  Gly Pro Val Val Pro Ala Trp Ser Gly Pro Arg Glu Ala Pro Asp Ser

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210      290      295      300
211 Leu Phe Ala Val Arg Arg His Leu Trp Gly Ser His Gly Asn Ser Thr
212 305      310      315      320
213 Phe Pro Glu Phe Leu His Asn Met Asp Tyr Phe Lys Phe His Asn Met
214      325      330      335
215 Arg Pro Pro Phe Thr Tyr Ala Thr Leu Ile Arg Trp Ala Ile Leu Glu
216      340      345      350
217 Ala Pro Glu Lys Gln Arg Thr Leu Asn Glu Ile Tyr His Trp Phe Thr
218      355      360      365
219 Arg Met Phe Ala Phe Phe Arg Asn His Pro Ala Thr Trp Lys Asn Ala
220      370      375      380
221 Ile Arg His Asn Leu Ser Leu His Lys Cys Phe Val Arg Val Glu Ser
222 385      390      395      400
223 Glu Lys Gly Ala Val Trp Thr Val Asp Glu Leu Glu Phe Arg Lys Lys
224      405      410      415
225 Arg Ser Gln Arg Pro Ser Arg Cys Ser Asn Pro Thr Pro Gly Pro
226      420      425      430
228 <210> SEQ ID NO: 5
229 <211> LENGTH: 23
230 <212> TYPE: DNA
231 <213> ORGANISM: Artificial Sequence
233 <220> FEATURE:
234 <223> OTHER INFORMATION: Primer for generation of mouse Fkh cDNA
236 <400> SEQUENCE: 5
237 gcagatctcc tgactctgcc ttc
239 <210> SEQ ID NO: 6
240 <211> LENGTH: 23
241 <212> TYPE: DNA
242 <213> ORGANISM: Artificial Sequence
244 <220> FEATURE:
245 <223> OTHER INFORMATION: Primer for generation of mouse Fkh cDNA
247 <400> SEQUENCE: 6
248 gcagatctga caagctgtgt ctg
250 <210> SEQ ID NO: 7
251 <211> LENGTH: 21
252 <212> TYPE: DNA
253 <213> ORGANISM: Artificial Sequence
255 <220> FEATURE:
256 <223> OTHER INFORMATION: Primer for generation of human Fkh cDNA
258 <400> SEQUENCE: 7
259 agcctgccct tggacaagga c
261 <210> SEQ ID NO: 8
262 <211> LENGTH: 21
263 <212> TYPE: DNA
264 <213> ORGANISM: Artificial Sequence
266 <220> FEATURE:
267 <223> OTHER INFORMATION: Primer for generation of human Fkh cDNA
269 <400> SEQUENCE: 8
270 gcaagacagt ggaaacctca c

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/696,867

DATE: 07/31/2002
TIME: 14:43:12

Input Set : A:\501d6.app
Output Set: N:\CRF3\07312002\I696867.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:13; N Pos. 3,6,9,12,15

Seq#:14; N Pos. 1,7,10,13,16,19